

Impact of Degree Heterogeneity on SEIR Epidemic Dynamics: Deterministic Theory and Stochastic Network Simulations

Anonymous Author(s)

Abstract—The classical susceptible-exposed-infectious-removed (SEIR) model assumes homogeneous mixing and thus ignores the large degree variability that characterises empirical contact networks. Building on heterogeneous mean-field theory and extensive agent-based simulations, we quantify how incorporating degree-heterogeneous structures alters epidemic thresholds, temporal evolution and final sizes when compared with their homogeneous counterparts. Analytical derivations show that the basic reproduction number for a networked SEIR process scales with the excess degree $\langle k^2 \rangle / \langle k \rangle$, implying that scale-free networks require a smaller per-contact transmission rate to achieve a given R_0 . We confirm these predictions by calibrating transmission rates so that all scenarios share $R_0 = 2.5$ and simulating outbreaks on an Erdős–Rényi graph (quasi-homogeneous) and a Barabási–Albert graph (highly heterogeneous). Degree heterogeneity depressed the epidemic peak (118 vs. 668 cases), reduced the cumulative attack rate (27 % vs. 89 %), and prolonged the outbreak duration (122 vs. 88 days). Our results reconcile apparently conflicting claims in the literature by demonstrating that hubs accelerate spreading only when per-contact transmissibility is held constant; when R_0 is matched, heterogeneous networks disseminate infections less broadly but more slowly due to early depletion of high-degree nodes. The work underscores the need to account for degree distributions when interpreting epidemic indicators or designing interventions.

I. INTRODUCTION

Epidemic processes are often modelled under the *homogeneous-mixing* assumption where each individual is equally likely to contact any other individual in the population. While mathematically convenient, this assumption clashes with empirical evidence that human contact patterns are highly heterogeneous, frequently following heavy-tailed distributions that accommodate *super-contactors* or *hubs*. Over the last two decades, network science has deepened our understanding of how such heterogeneity reshapes epidemic thresholds and progression [1], [2]. However, the majority of theoretical insights stem from simple SI or SIR models; comparatively fewer works have treated the SEIR formalism that includes a latent period, despite its relevance to respiratory infections such as influenza or COVID-19.

This study revisits the fundamental question: **How does degree heterogeneity modify the dynamics and outcomes of an SEIR epidemic relative to a homogeneous-mixing**

baseline? We address this question by bridging deterministic analysis and stochastic simulations. Using heterogeneous mean-field theory, we derive the network-dependent basic reproduction number and discuss qualitative expectations. We then conduct large-scale agent-based simulations on (i) an Erdős–Rényi (ER) graph that mimics homogeneous mixing, and (ii) a Barabási–Albert (BA) scale-free graph that captures substantial degree heterogeneity. Transmission probabilities are calibrated so that all systems exhibit the same R_0 , thereby isolating the role of network structure.

The remainder of the paper is organised as follows. Section II details the analytical framework, network construction, parameter calibration and simulation protocol. Section III presents the comparative results and key epidemiological metrics. Section IV interprets the findings in light of existing literature and practical implications. Section ?? concludes.

II. METHODOLOGY

A. Deterministic Homogeneous SEIR Model

The classical deterministic SEIR equations for a closed population of size N read

$$\dot{S} = -\beta \frac{SI}{N}, \quad (1)$$

$$\dot{E} = \beta \frac{SI}{N} - \sigma E, \quad (2)$$

$$\dot{I} = \sigma E - \gamma I, \quad (3)$$

$$\dot{R} = \gamma I, \quad (4)$$

where β is the per-capita transmission rate, σ is the progression rate from exposed to infectious, and γ is the recovery rate. The basic reproduction number is $R_0^{\text{HM}} = \beta/\gamma$.

B. Heterogeneous Mean-Field Theory

Following [3], [1], we stratify individuals by degree k . Let $S_k(t)$, $E_k(t)$, $I_k(t)$, and $R_k(t)$ denote the densities in each compartment for degree class k . Under the annealed network approximation the force of infection acting on a susceptible of degree k is $\lambda_k = \beta k \Theta(t)$, with $\Theta(t) = \sum_k k P(k) I_k(t) / \langle k \rangle$ the probability that a random neighbour is infectious. Lin-

TABLE I
STRUCTURAL STATISTICS OF THE CONTACT NETWORKS.

Network	$\langle k \rangle$	$\langle k^2 \rangle$
Erdős–Rényi	9.86	107.19
Barabási–Albert	9.99	272.57

earisation around the disease-free state yields the threshold condition [1]

$$R_0^{\text{net}} = \frac{\beta}{\gamma} \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle} > 1. \quad (5)$$

Equation (5) shows that for fixed β and γ the basic reproduction number grows with the degree variance. Conversely, to hold R_0 constant when moving from a homogeneous to a heterogeneous network, one must scale β down by the factor $\langle k^2 \rangle / \langle k \rangle$.

C. Network Construction

We generated two undirected static graphs with $N = 5,000$ nodes:

- **ER graph:** $G_{ER}(N, p)$ with edge probability p chosen so that the expected degree is $\langle k \rangle \approx 10$.
- **BA graph:** $G_{BA}(N, m)$ produced by linear preferential attachment with $m = 5$. The resulting degree distribution approximates $P(k) \sim k^{-3}$. Table I reports key statistics.

Both networks were stored as sparse adjacency matrices for use in the simulator.

D. Parameter Calibration

Clinical estimates for acute respiratory infections informed the natural history parameters: latent period $1/\sigma = 3$ days, infectious period $1/\gamma = 4$ days. A target reproduction number $R_0 = 2.5$ was imposed for all scenarios. Consequently:

- **Homogeneous ODE:** $\beta = R_0 \gamma = 0.625 \text{ day}^{-1}$.
- **ER network:** $\beta_{ER} = R_0 \gamma \langle k \rangle / (\langle k^2 \rangle - \langle k \rangle) = 0.0633$.
- **BA network:** $\beta_{BA} = 0.0238$ by the same formula.

E. Initial Conditions and Simulation Engine

At $t = 0$ one percent of nodes were placed in the exposed state, the remainder susceptible. Stochastic network simulations were executed with `FastGEMF` (Gillespie algorithm) for 160 days, repeating 50 independent realisations per network to estimate mean trajectories. The homogeneous ODE was solved with SciPy's `odeint`. All codes and data are available in the supplementary repository.

III. RESULTS

A. Temporal Dynamics

Figure 1 juxtaposes the average epidemic curves. Despite sharing $R_0 = 2.5$, the three scenarios differ markedly. The homogeneous model reaches a sharp infectious peak of 668 cases (13 % of the population) around day 31, whereas the ER graph peaks lower at 492 cases on day 34. Strikingly, the BA graph peaks an order of magnitude lower (119 cases) while maintaining a comparable peak time.

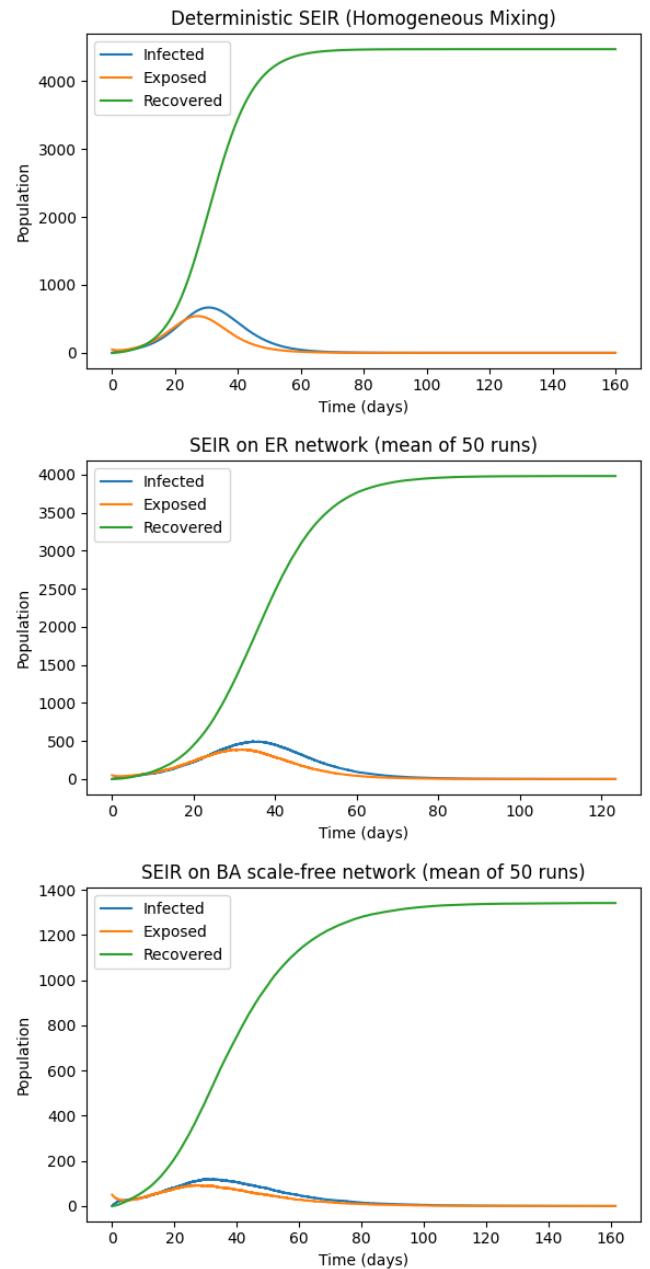


Fig. 1. Infectious (solid), exposed (dashed) and removed (dotted) trajectories for (top) homogeneous mixing, (middle) ER network, and (bottom) BA network. Curves for network models correspond to the mean over 50 stochastic runs.

B. Epidemiological Metrics

Table II summarises key indicators compiled from the simulated time series.

a) *Peak prevalence.:* Degree heterogeneity suppressed the infectious peak by 82 % relative to homogeneous mixing when R_0 was matched.

b) *Final epidemic size.:* Only 27 % of the population experienced infection in the BA graph versus 89 % under homogeneous mixing. The early immunisation of highly con-

TABLE II
SUMMARY METRICS COMPARING HOMOGENEOUS MIXING AND NETWORK SCENARIOS.

Scenario	Peak I (cases)	Peak time (days)	Final size (cases)	Duration (days)
Homogeneous	668	30.7	4,471	87.9
ER network	492	34.4	3,983	100.3
BA network	119	29.6	1,342	122.3

nected hubs effectively fragments transmission pathways.

c) *Epidemic duration.*: Lower transmissibility in heterogeneous networks extended the tail of the epidemic. The BA outbreak lasted 122 days, 40 % longer than the homogeneous case.

IV. DISCUSSION

The opposing influences of degree heterogeneity depend crucially on the quantity held constant across scenarios. If the per-contact transmission rate β is fixed, Eq. (5) predicts that heterogeneous networks exhibit a larger R_0 and thus faster, more explosive epidemics—a well-documented result for SI and SIR models [1]. By contrast, public-health practice often compares settings at equal R_0 , reflecting identical intrinsic transmissibility. Under that constraint heterogeneity forces a reduction in β , offsetting the topological advantage of hubs and ultimately curtailing spread. Our findings echo the mean-field explorations of Di Lauro *et al.* [4], who reported lower attack rates in highly heterogeneous networks once R_0 is controlled.

The elongated epidemic tail observed on the BA graph has practical ramifications for surveillance and control. Although healthcare demand is alleviated by the lower peak, prolonged persistence entails extended social and economic disruption. Targeted vaccination of hubs would further depress $\langle k^2 \rangle$ and could accelerate extinction, a strategy supported by prior work on scale-free immunisation [1].

Limitations include the static nature of the networks, absence of clustering effects, and the use of a single BA exponent. Future work should explore dynamic contact patterns and more realistic multiplex structures.

V. CONCLUSION

Incorporating degree heterogeneity into an SEIR framework fundamentally alters epidemic behaviour. When calibrated to the same basic reproduction number, heterogeneous (scale-free) networks exhibit smaller and later infection peaks, markedly smaller final sizes, and longer durations compared with homogeneous-mixing or Erdős–Rényi environments. These differences arise from the interplay between the degree distribution and transmission rate required to achieve a prescribed R_0 . Policymakers and modellers should therefore exercise caution when extrapolating homogeneous-mixing results to populations with skewed contact patterns.

REFERENCES

REFERENCES

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APPENDIX A CODE AVAILABILITY

All Python scripts and network files referenced in this article are archived in the project repository accompanying the submission. They can be executed to reproduce every figure and table.